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## RAW SEQUENCE LISTING

DATE: 10/05/2001

PATENT APPLICATION: US/09/955,526

TIME: 15:25:48

Input Set : A:\LJ4868.txt

Output Set: N:\CRF3\10052001\I955526.raw

4 <110> APPLICANT: Reed, John C.  
 6 <120> TITLE OF INVENTION: Plant Cytoprotective Genes and Methods  
 7 of Using Same  
 9 <130> FILE REFERENCE: P-LJ 4868  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/955,526  
 C--> 11 <141> CURRENT FILING DATE: 2001-09-12  
 11 <150> PRIOR APPLICATION NUMBER: US 09/661,014  
 12 <151> PRIOR FILING DATE: 2000-09-13  
 14 <160> NUMBER OF SEQ ID NOS: 7  
 16 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 617  
 20 <212> TYPE: DNA  
 21 <213> ORGANISM: Lycopersicon esculentum  
 23 <220> FEATURE:  
 24 <221> NAME/KEY: CDS  
 25 <222> LOCATION: (103)...(594)  
 27 <400> SEQUENCE: 1  
 28 cgttctctga tgcgtagctg aagaaatatt accggaaagt tcacaggaaa taagtggcgg 60  
 29 cgggtgcgtgg ctcttggtga ataccaagcg agaggagata ag atg ccg gaa cat 114  
 30 Met Pro Glu His  
 31 1  
 33 cct gct gca gac tca tca gcc acc gac aac acc gtc acc gtc aag cgt 162  
 34 Pro Ala Ala Asp Ser Ser Ala Thr Asp Asn Thr Val Thr Val Lys Arg  
 35 5 10 15 20  
 37 tat gcc cct ccc aat cag cgg aat cgt tca ctc ggc agg cga aaa tct 210  
 38 Tyr Ala Pro Pro Asn Gln Arg Asn Arg Ser Leu Gly Arg Arg Lys Ser  
 39 25 30 35  
 41 gga gat cga ctt gaa aga gct agc agc tat gct agt gat gga gag aag 258  
 42 Gly Asp Arg Leu Glu Arg Ala Ser Ser Tyr Ala Ser Asp Gly Glu Lys  
 43 40 45 50  
 45 aac caa atg aga gca gct aag tct gta tct gat gct gga gtc aat cga 306  
 46 Asn Gln Met Arg Ala Ala Lys Ser Val Ser Asp Ala Gly Val Asn Arg  
 47 55 60 65  
 49 gta aat gat tat cct cca aca aag tta ata ccg cta caa gga tgt tgt 354  
 50 Val Asn Asp Tyr Pro Pro Thr Lys Leu Ile Pro Leu Gln Gly Cys Cys  
 51 70 75 80  
 53 aca agc gaa gct ttt cag cta cta aat gac cgc tgg gca gct gct ctg 402  
 54 Thr Ser Glu Ala Phe Gln Leu Leu Asn Asp Arg Trp Ala Ala Ala Leu  
 55 85 90 95 100  
 57 aat gct cat aat aat tta tca gaa gat tct cgt gaa agg cct gta atg 450  
 58 Asn Ala His Asn Asn Leu Ser Glu Asp Ser Arg Glu Arg Pro Val Met  
 59 105 110 115  
 61 tac aca aaa aga tca cct tgg ggg cat cct ttt ctt cca cat caa ttg 498  
 62 Tyr Thr Lys Arg Ser Pro Trp Gly His Pro Phe Leu Pro His Gln Leu  
 63 120 125 130  
 65 atg tca caa gca gga gct gaa tct tct act ggc cag aag gat ttt cta 546

ENTERED

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66 Met Ser Gln Ala Gly Ala Glu Ser Ser Thr Gly Gln Lys Asp Phe Leu
67      135                      140                      145
69 agc aaa ctt cag atg gct atg ctc aat aca cat gtc aat ttc gat gcc 594
70 Ser Lys Leu Gln Met Ala Met Leu Asn Thr His Val Asn Phe Asp Ala
71      150                      155                      160
73 taaatgctat ccatcaagtg gtc 617
75 <210> SEQ ID NO: 2
76 <211> LENGTH: 164
77 <212> TYPE: PRT
78 <213> ORGANISM: Lycopersicon esculentum
80 <400> SEQUENCE: 2
81 Met Pro Glu His Pro Ala Ala Asp Ser Ser Ala Thr Asp Asn Thr Val
82 1      5      10      15
83 Thr Val Lys Arg Tyr Ala Pro Pro Asn Gln Arg Asn Arg Ser Leu Gly
84      20      25      30
85 Arg Arg Lys Ser Gly Asp Arg Leu Glu Arg Ala Ser Ser Tyr Ala Ser
86      35      40      45
87 Asp Gly Glu Lys Asn Gln Met Arg Ala Ala Lys Ser Val Ser Asp Ala
88      50      55      60
89 Gly Val Asn Arg Val Asn Asp Tyr Pro Pro Thr Lys Leu Ile Pro Leu
90 65      70      75      80
91 Gln Gly Cys Cys Thr Ser Glu Ala Phe Gln Leu Leu Asn Asp Arg Trp
92      85      90      95
93 Ala Ala Ala Leu Asn Ala His Asn Asn Leu Ser Glu Asp Ser Arg Glu
94      100     105     110
95 Arg Pro Val Met Tyr Thr Lys Arg Ser Pro Trp Gly His Pro Phe Leu
96      115     120     125
97 Pro His Gln Leu Met Ser Gln Ala Gly Ala Glu Ser Ser Thr Gly Gln
98      130     135     140
99 Lys Asp Phe Leu Ser Lys Leu Gln Met Ala Met Leu Asn Thr His Val
100 145     150     155     160
101 Asn Phe Asp Ala
105 <210> SEQ ID NO: 3
106 <211> LENGTH: 1034
107 <212> TYPE: DNA
108 <213> ORGANISM: Lycopersicon esculentum
110 <220> FEATURE:
111 <221> NAME/KEY: CDS
112 <222> LOCATION: (87)...(830)
114 <221> NAME/KEY: misc_feature
115 <222> LOCATION: (1)...(1034) ✓
116 <223> OTHER INFORMATION: n = A,T,C or G
118 <400> SEQUENCE: 3
119 gagcaaacat aacattgtct acgttcagat aaatatcctt tgctcatttc agttccaaaa 60
120 actcgaagaa gaagaagaag agaaca atg gaa ggt ttc aca tcg ttc ttc gac 113
121      Met Glu Gly Phe Thr Ser Phe Phe Asp
122      1      5
124 tcg caa tct gcc tct cgc aac cgc tgg agt tat gat tct ctc aaa aac 161
125 Ser Gln Ser Ala Ser Arg Asn Arg Trp Ser Tyr Asp Ser Leu Lys Asn

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126 10          15          20          25
128 ttc cgc cag atc tca cct ctc gtt caa act cat ctc aag cag gtg tac 209
129 Phe Arg Gln Ile Ser Pro Leu Val Gln Thr His Leu Lys Gln Val Tyr
130          30          35          40
132 ctt acg cta tgc tgt gct tta gtg gca tcg gct gct ggg gct tac ctt 257
133 Leu Thr Leu Cys Cys Ala Leu Val Ala Ser Ala Ala Gly Ala Tyr Leu
134          45          50          55
136 cac att cta tgg aat atc ggt ggc ctc ctc aca aca atg gct tgc atg 305
137 His Ile Leu Trp Asn Ile Gly Gly Leu Leu Thr Thr Met Ala Cys Met
138          60          65          70
140 gga agc atg gtg tgg ctt ctc tca gct cct cct tat caa gag caa aaa 353
141 Gly Ser Met Val Trp Leu Leu Ser Ala Pro Pro Tyr Gln Glu Gln Lys
142          75          80          85
144 agg gtg gct ctt ctg atg gca gct gca ctt ttt gaa ggc gcc tct att 401
145 Arg Val Ala Leu Leu Met Ala Ala Ala Leu Phe Glu Gly Ala Ser Ile
146 90          95          100          105
148 ggt cct ctg att gag ctg ggc att aac ttc gat cca agc att gtg ttt 449
149 Gly Pro Leu Ile Glu Leu Gly Ile Asn Phe Asp Pro Ser Ile Val Phe
150          110          115          120
152 ggc gct ttt gta ggt tgt gct gtg gtt ttt ggt tgc ttc tca gct gct 497
153 Gly Ala Phe Val Gly Cys Ala Val Val Phe Gly Cys Phe Ser Ala Ala
154          125          130          135
156 gcc atg ttg gca agg cgc agg gag tac ttg tac ctc ggg ggc ctt ctt 545
157 Ala Met Leu Ala Arg Arg Arg Glu Tyr Leu Tyr Leu Gly Gly Leu Leu
158          140          145          150
160 tca tct ggc gtc tcc ctt ctc ttc tgg ttg cac ttt gca tcc tcc att 593
161 Ser Ser Gly Val Ser Leu Leu Phe Trp Leu His Phe Ala Ser Ser Ile
162          155          160          165
164 ttt ggt ggt tcc atg gct gtt ttc aag ttt gag ttg tat ttt gga ctc 641
165 Phe Gly Gly Ser Met Ala Val Phe Lys Phe Glu Leu Tyr Phe Gly Leu
166 170          175          180          185
168 ttg gtg ttt gtg ggc tac atc gtc ttt gac acc caa gaa att att gag 689
169 Leu Val Phe Val Gly Tyr Ile Val Phe Asp Thr Gln Glu Ile Ile Glu
170          190          195          200
172 aag gct cac ttg ggt gat atg gat tac gtt aag cat gca ttg acc ctt 737
173 Lys Ala His Leu Gly Asp Met Asp Tyr Val Lys His Ala Leu Thr Leu
174          205          210          215
176 ttc aca gat ttt ggc gct gtt ttt gtg cgg att ctg atc atc atg tta 785
177 Phe Thr Asp Phe Gly Ala Val Phe Val Arg Ile Leu Ile Ile Met Leu
178          220          225          230
180 aag aat gca tct gag aag gaa gag aag aag aag aag agg aga aac 830
181 Lys Asn Ala Ser Glu Lys Glu Glu Lys Lys Lys Lys Arg Arg Asn
182          235          240          245
W--> 184 tagatttgct tctcaacttg tggtttccan aactccttgt gttcacctga aacaagcatg 890
185 ttaatatgtt gatacttgct tcacttttagc ataggtgtg atgtaatgtc gtgtgacatg 950
186 ccattatggc tgtgtgattg agcatctagc ctttttatct tctaaagctt ttttcttaac 1010
187 attgataagg aaagttcctt gtga 1034
189 <210> SEQ ID NO: 4
190 <211> LENGTH: 248

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191 <212> TYPE: PRT
192 <213> ORGANISM: Lycopersicon esculentum
194 <400> SEQUENCE: 4
195 Met Glu Gly Phe Thr Ser Phe Phe Asp Ser Gln Ser Ala Ser Arg Asn
196 1 5 10 15
197 Arg Trp Ser Tyr Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro Leu
198 20 25 30
199 Val Gln Thr His Leu Lys Gln Val Tyr Leu Thr Leu Cys Cys Ala Leu
200 35 40 45
201 Val Ala Ser Ala Ala Gly Ala Tyr Leu His Ile Leu Trp Asn Ile Gly
202 50 55 60
203 Gly Leu Leu Thr Thr Met Ala Cys Met Gly Ser Met Val Trp Leu Leu
204 65 70 75 80
205 Ser Ala Pro Pro Tyr Gln Glu Gln Lys Arg Val Ala Leu Leu Met Ala
206 85 90 95
207 Ala Ala Leu Phe Glu Gly Ala Ser Ile Gly Pro Leu Ile Glu Leu Gly
208 100 105 110
209 Ile Asn Phe Asp Pro Ser Ile Val Phe Gly Ala Phe Val Gly Cys Ala
210 115 120 125
211 Val Val Phe Gly Cys Phe Ser Ala Ala Ala Met Leu Ala Arg Arg Arg
212 130 135 140
213 Glu Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Val Ser Leu Leu
214 145 150 155 160
215 Phe Trp Leu His Phe Ala Ser Ser Ile Phe Gly Gly Ser Met Ala Val
216 165 170 175
217 Phe Lys Phe Glu Leu Tyr Phe Gly Leu Leu Val Phe Val Gly Tyr Ile
218 180 185 190
219 Val Phe Asp Thr Gln Glu Ile Ile Glu Lys Ala His Leu Gly Asp Met
220 195 200 205
221 Asp Tyr Val Lys His Ala Leu Thr Leu Phe Thr Asp Phe Gly Ala Val
222 210 215 220
223 Phe Val Arg Ile Leu Ile Ile Met Leu Lys Asn Ala Ser Glu Lys Glu
224 225 230 235 240
225 Glu Lys Lys Lys Lys Arg Arg Asn
226 245
229 <210> SEQ ID NO: 5
230 <211> LENGTH: 28
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: primer
237 <400> SEQUENCE: 5
238 ggaattcatg gaaggtttca catcgttc 28
240 <210> SEQ ID NO: 6
241 <211> LENGTH: 43
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: primer

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248 <400> SEQUENCE: 6  
249 ccgctcgagc tagggtcgac tgttttctcct cttcttcttc ttc 43  
251 <210> SEQ ID NO: 7  
252 <211> LENGTH: 28  
253 <212> TYPE: DNA  
254 <213> ORGANISM: Artificial Sequence  
256 <220> FEATURE:  
257 <223> OTHER INFORMATION: primer  
259 <400> SEQUENCE: 7  
260 ggaattcatg ccggaacatc ctgctgca 28